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(57) Abstract

This invention relates to human immunodeficiency virus (HIV) protein fragments which have antiviral activity, and particularly relates to HIV peptides derived from the HIV transmembrane glycoprotein (gp41) which inhibit HIV-induced cell-cell fusion. This invention further relates to methods for the inhibition of enveloped viral infection, and to methods that modulate biochemical processes which involve coiled coil peptide interactions.

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COMPOUNDS WHICH INHIBIT HIV REPLICATION

The present invention was made with Government support under grants numbers R01-AI30411 and P30-AI28662 from the National Institute of Allergy & Infectious Diseases. The Government has certain rights to this invention.

This application is a continuation-in-part of co-pending application Serial No. 07/927,532 of C. Wild, T. Matthews and D. Bolognesi, filed 7 August 1992, the disclosure of which is to be incorporated by reference herein in its entirety.

1. Introduction

This invention relates to human immunodeficiency virus (HIV) protein fragments which have antiviral activity, and particularly relates to HIV peptides derived from the HIV transmembrane glycoprotein (gp41) which inhibit HIV-induced cell-cell fusion. This invention further relates to methods for the inhibition of enveloped viral infection, and to methods that modulate biochemical processes which involve coiled coil peptide interactions.

2. Background of the Invention

Numerous HIV protein fragments, or peptides, have been identified in an effort to develop an effective HIV vaccine. See generally B. Spalding, Biotechnology 10, 24 (Jan. 1992). Examples of patent applications which are directed to antigenic epitopes of the gp41 protein include J. Rosen et al., PCT Application WO 87/06005 and R. Duncan, EPO Application 0 371 817. To date, the development of an anti-HIV vaccine has been difficult.

N. Qureshi et al., Aids 1990 4, 553-558, describe a segment of the HIV transmembrane protein (designated "gp41") which inhibits T-cell activation in vitro. This segment, designated "CS3", when conjugated to human serum albumin and labeled with fluorescein, binds specifically to CD4+ cell lines, and is said to have antiviral activity. CS3 comprises amino acids 581 to 597 of the gp41 protein.

B. Kemp et al., EPO Application 0 323 157, describes a fragment comprised of amino acids 572 to 591 of the gp41 protein which is said to have antiviral activity.

3. Summary of the Invention

A first aspect of the present invention is a peptide selected from the group consisting of: (a) the peptide DP-107, which has the formula, from amino terminus to carboxy terminus, of:

NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ

(SEQ ID NO: 1); and (b) peptides of from 14 to 60 amino acids in length which form a heterodimer with the peptide DP-107 (SEQ ID NO: 1) (hereinafter on occasion referred to as "active compounds").

A second aspect of the present invention is a process for inhibiting HIV-induced cell fusion. The process comprises contacting to an HIV-infected cell an effective fusion-inhibiting amount of a peptide selected from the group consisting of: (a) the peptide DP-107, which has the formula, from amino terminus to carboxy terminus, of:

NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ

(SEQ ID NO: 1); and (b) peptides of from about 14 to 60 amino acids in length which form a heterodimer with the peptide DP-107 (SEQ ID NO: 1).

A third aspect of the present invention is a process for testing compounds for the ability to inhibit the ability of HIV to infect cells. The process comprises (a) contacting a test compound to a multimer of a peptide selected from the group consisting of: (i) the peptide DP-107, which has the formula, from amino terminus to carboxy terminus of:

NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ

(SEQ ID NO: 1) ; and (ii) peptides of from 14 to 60 amino acids in length which form a heterodimer with the peptide DP-107 (SEQ ID NO: 1); and then (b) detecting whether the test compound disrupts said multimer, the ability of the test compound to disrupt the multimer indicating the test compound is capable of inhibiting HIV infection of cells.

A further aspect of the invention is a method for inhibiting enveloped viral infection comprising contacting an uninfected cell with an effective amount of a peptide capable of contributing to the formation of a coiled coil peptide structure so that an enveloped virus is inhibited from infecting the uninfected cell.

The foregoing and other objects and aspects of the present invention are explained in detail in the drawings herein and the specification set forth below.

4. Brief Description of the Drawings

Figure 1 shows the sequences of various peptides studied. In DP-107 (SEQ ID NO: 1), DP-121 (SEQ ID NO: 2), and DP-125 (SEQ ID NO: 3) the leucine or isoleucine heptad repeat units are underlined. DP-107, DP-121, and DP-125 are acetylated at the NH_2 terminus and amidated at the COOH terminus. DP-116 (SEQ ID NO:4) (identical to the CS3 peptide) is amidated at the carboxy terminus and has a free amine

terminus. DP-31 (SEQ ID NO: 5) is neither acetylated nor amidated. Amino acid residues are numbered according to Human Retroviruses and AIDS (1991).

Figure 2 shows the CD spectra of 10 mM solutions of DP-107(m), DP-121(+), and DP-116(1) at 0°C (A) and 37°C (B). Concentration dependence of the midpoint of the temperature dependence (T_m) of the CD signal (C). T_m corresponds to the maxima of the first derivative of the CD melt curve. The CD spectra were obtained in 10mM sodium phosphate, 150mM sodium chloride buffer at pH 7.0.

Figure 3 shows the test for peptide blockade of AA5 cell infection by HIV- 1_{LAI} About 500 $TCID_{50}$ HIV-LAI were added to $2x10^4$ AA5 cells and test peptides (final concentrations shown) in a final volume of 100 ml. Cell cultures were maintained in 96-well microtiter plates for 8 days by addition of fresh medium (but no further addition of peptides) every other day. On the eighth day post-infection, supernatant was tested for reverse transcriptase activity as evidence of successful infection.

Figure 4 shows the test for direct virocidal effect of peptides and soluble CD4 (sT4) The HIV-1_{LAI} virus stock was divided into two portions. Samples of one portion (shown in figure as virus pelleted +) were treated for 2 hr at 37°C in medium alone, with DP-107 at 40 mg/ml, or with sT4 at 10 mg/ml. Virus was then pelleted through a 5% sucrose layer to separate virus from non-associated inhibitor. The virus-containing pellets were dispersed in media and serial dilutions tested for infectivity on the AA5 cells. Serial four fold dilutions of the other portion of virus (virus pelleted -) were tested directly for infection of the cells with each dilution of virus incubated in the absence or presence of DP-107 at 40 mg/ml.

Figure 5 shows a comparison of peptides and soluble CD4 to inhibit primary virus isolates. About 25 $TCID_{100}$ of two primary isolates and $HIV\text{-}1_{LAI}$ were added to PRA activated human PBMCs (about $1.5x10^6$/ml) containing the indicated final concentrations of test peptide or 5T4. Each treatment condition was tested in duplicate and the cells were cultured in RPMI1640 containing 10% FCS 5% IL2. Four days post infection an equal number of fresh PBMCs were added to each well. This step allows for further expansion of virus and increases the noise to background ratio in the final RT assay. Supernatant was harvested 8 days after infection and tested for the presence of reverse transcriptase activity.

5. Detailed Description of the Invention

The term "HIV" as used herein refers to HIV-1, and the numbering of amino acids in HIV proteins and fragments thereof given herein is with respect to the $HIV1_{LAI}$ isolate. It is to be understood, however, that while HIV viral infection and the effects of DP-107 on such HIV infection are being used herein as a model systems in which the potential anti-viral properties of peptides capable of forming coiled coils are described, such properties of coiled coil peptides may represent generalized mechanisms by which a broad spectrum of enveloped viral infections may be inhibited. Enveloped viruses whose infectivity may be inhibited using the coiled coil peptides of the invention may include, but are not limited to, other HIV strains such as HIV-2, as well as influenza viruses, syncytial respiratory viruses, an herpes viruses.

The DP107 peptide sequence is based on a highly conserved region in the transmembrane protein (TM)

which was predicted by Gallaher et al., AIDS Res. and Human Retro. 5, 431 (1989), to form an extended amphipathic α-helix with structural analogues in the TM proteins of several fusogenic viruses such as influenza and other retroviruses. The function of the site is not known but may be related to multimerization of the envelope glycoprotein. The site has been shown to contain a "leucine zipper" repeat. See E. Delwart et al., AIDS Res. and Human Retro. 6, 703 (1990). The use of peptides such as DP-107 capable of forming coiled coils, therefore, may serve to interfere, block, or in some way modulate many biochemical processes which involve such coiled coil peptide formations. Such biochemical process may include, but are not limited to transcription factors (Abel and Maniatis, Nature 341:24) and physiological processes involving membrane fusion (White, J.M., 1992, Science 258:1917-1924).

The biological activity of the peptide DP-107 was unexpected and its mechanism is not readily apparent. The results shown herein suggest that it does not act directly on the cell-free virions. Qureshi et al. (AIDS 4, 553 (1990)) have reported that an overlapping peptide, CS3 (DP-116 herein), inhibited infection when coupled to albumin and suggested that this occurred by attachment to a second receptor on the cell surface required for membrane fusion. These investigators have tentatively identified a candidate for the receptor as a 44 kD protein. Although such a mechanism would be consistent with the DP-107 result shown in Fig. 4 described hereinbelow, other observations argue that these two peptides are quite dissimilar and as such might function through different mechanisms. Most importantly, the CS3 peptide was only active after conjugation to albumin

which contrasts with the striking anti-viral effect of the free (non-conjugated) DP-107 peptide. Also, the CS3 peptide showed no evidence for stable secondary structure by CD even at low temperatures and high concentrations. Our experiments indicate that structure or capacity to assume stable secondary structure is a requirement for biological activity. For example, the DP-107 analogue containing a helix breaking proline substitution (DP-121) and several truncated versions of DP-107 (not shown) that either disrupted or failed to show stable solution structure did not exhibit anti-viral activity.

As noted above, a first aspect of the present invention is a peptide selected from the group consisting of:

(a) the peptide DP-107, which has the formula, from amino terminus to carboxy terminus, of: NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ (SEQ ID NO:1); and

(b) peptides of from 14 to 60 amino acids in length which form a heterodimer with the peptide DP-107 (SEQ ID NO:I).

In general, the peptide may be of any suitable length, but is preferably from 14 to 60 amino acids in length, and more preferably from 16 to 38 amino acids in length. In addition, it will be appreciated that minor variations can be made to the peptide. For example, the peptide may be acetylated at the amino terminus thereof and/or amidated at the carboxy terminus thereof.

Peptides of the invention may be provided as multimers, particularly as dimers and tetramers. When provided in such form the multimer may be stabilized by covalently joining the monomers to one another. For example, a cysteine residue may be added to

either (or both) ends of the monomer and monomers of the multimer covalently joined to one another by a disulfide bond between cysteine residues. Reactions are carried out in accordance with known techniques. In this manner two monomers of a dimer may be covalently joined to form a covalently stabilized dimer, and if desired two such covalently stabilized dimers conjugated to one another to form a tetramer. In another example, all four members of a tetramer could be covalently joined to one another through disulfide linkages between terminally positioned cysteine residues.

Other techniques for stabilizing the multimeric forms of these peptides include crosslinking the monomer components to one another through the formation of intermolecular amide bonds. This process involves the reaction of the amine moiety of a basic amino acid residue i.e. lysine, with the carboxy moiety of an acidic amino acid residue i.e. aspartic or glutamic acid.

Several techniques can used to determine the multimerization state of a given peptide or peptide mixture (homodimer or heterodimer). The most straightforward methods involve determining the apparent molecular weight of the multimer complex and from this determining the number of associated monomer components (this can be accomplished by dividing this apparent molecular weight by the molecular weight of the monomer). Analytical ultracentrifugation is a particularly suitable technique for this purpose. The specifics of this method are known to those skilled in the art. See., e.g., P. Graceffa et al., J. Biol. Chem. 263, 14196-14202 (1988), and can be summarized as follows. The material of interest is placed in a sample cell and spun very rapidly in a model E

ultracentrifuge equipped with the appropriate detection devices. Information collected during the experiment combined with the amino acid composition of the peptide allows for the determination of the apparent MW of the multimer complex. Fast Protein Liquid Chromatography (FPLC) can also be used for this purpose. This technique is different from the above in that, as a type of chromatography, it ultimately requires reference back to some primary standard (determined by analytical ultracentrifugation). Pharmica Biosystems supplies the SUPERDEX 75™ column, which allows for the separation of the various multimeric forms of self-associating peptides. These determinations are carried out under non-denaturing (native) conditions and when referenced to the appropriate standards can be used to identify peptide and protein oligomerization states.

As will also be apparent to those skilled in the art, the test for heterodimerization may be carried out using either of the above two methods or through the use of CD combined with one or the other of these methods. This latter technique, in brief, involves adding known amounts of peptide to a solution containing a known amount of either the same peptide (for homodimerization) or a different peptide (for heterodimerization) and following the CD signal as a function of this addition. An increase in the magnitude of the signal as peptide is added indicates that the added material is participating in multimer formation. Homo vs heterodimerization is determined by carrying out this same experiment using FPLC or ultracentrifugation, which would determine if the resulting system is either single (hetero) or multi (homo) component. A second, and particularly preferred, approach to this same end is to conduct a

CD melt on this same sample. If heterodimerization has occurred, then a single transition corresponding to the T_m of the heterodimer will be observed (this T_m value will probably be different from the value for either of the mixture components). If only homodimerization takes place then two transitions (two T_m's) will be observed.

A process for inhibiting HIV-induced cell fusion, as also disclosed herein, comprising contacting to an HIV-infected cell an effective fusion-inhibiting amount of a peptide as given above. The process may be carried out in vitro in an aqueous solution, or may be carried out in vivo in a cellular culture assay for HIV infection (e.g., the CEM-SS cell monolayer plaque assay described in L. Kucera et al., Aids Research and Human Retroviruses 6, 491 (1990) or in an animal subject afflicted with the HIV virus- The process may be carried out with peptides of the invention in the form of multimers (particularly dimers) thereof as discussed above. The process may be carried out in a human or animal subject to prevent HIV-induced cell fusion, in which case the compounds may be combined with a suitable pharmaceutically acceptable carrier (such as sterile, pyrogen-free physiological saline solution, or sterile, pyrogen free phosphate-buffered saline solution), and administered to the subject by a suitable route (i.e., by intramuscular injection, subcutaneous injection, or intravenous injection). The therapeutic dosage is about 1 to 10,000 μg/Kg of patient weight per day, more particularly from about 10 to 1,000 μg/Kg of patient weight per day, and most particularly about 100 μg/Kg of patient weight per day. Thus, the present invention provides a method of combatting HIV (and particularly HIV-induced cell fusion) in a human or animal subject by administering

an active compound as given herein in an effective in an effective HIV (or more particularly HIV-induced cell fusion)-combatting amount. The present invention also provides the use of an active compound as given herein for the preparation of a medicament for combatting HIV (or more particularly HIV-induced cell fusion) in a human or animal subject in need of such treatment.

A still further aspect of the present invention is a process, useful in rational drug design, for testing compounds for the ability to inhibit the ability of HIV to infect cells. The process comprises (a) contacting a test compound to a multimer (e.g., dimer, tetramer) of a peptide as given above, and then (b) detecting whether the test compound disrupts said multimer, the ability of said test compound to disrupt said multimer indicating the test compound is capable of inhibiting HIV infection of cells. This process is noteworthy for its ability to identify compounds directed to a site which has not heretofore been explored in rational drug design. The process may be conveniently carried out in vitro in an aqueous solution containing the multimer by adding the test compound to the aqueous solution, and then determining whether or not the multimer structure has been disrupted. Disruption of multimer structure may be determined in the same manner as set forth above.

Note that amino acid sequences disclosed herein are presented in the amino to carboxy direction, from left to right. The amino and carboxy groups are not presented in the sequence. Amino acids are represented herein by one letter code or three letter code as follows:

Ala; A=Alanine	Leu; L=Leucine
Arg; R=Arginine	Lys; K=Lysine

Asn; N=Asparagine	Met; M=Methionine
Asp; D=Aspartic acid	Phe; F=Phenylalanine
Cys; C=Cysteine	Pro; P=Proline
Gln; Q=Glutamine	Ser; S=Serine
Glu; E=Glutamic Acid	Thr; T=Threonine
Gly; G-=Glycine	Trp; W=Tryptophan
His; H=Histidine	Tyr; Y=Tyrosine
Ile; I=Isoleucine	Val; V=Valine

The foregoing abbreviations are in accordance with established usage. See, e.g., U.S. Patent No. 4,871,670 to Hudson et al. at Col. 3 lines 20-43 (applicants specifically intend that the disclosure of this and all other patent references cited herein be incorporated herein by reference).

The present invention is explained in greater detail in the following Examples. These Examples are for illustrative purposes only, and are not to be taken as limiting of the invention.

6. EXAMPLE: Peptide Synthesis

Peptides DP-107 (SEQ ID NO: 1) , DP121 (SEQ ID NO: 2), DP-125 (SEQ ID NO: 3), DP-116 (SEQ ID NO: 4), and DP-31 (SEQ ID NO: 5) were synthesized using FAST MOC™ chemistry on an Applied Biosystems Model 431A peptide synthesizer. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resins (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with TFA (10ml), H_2O (0. 5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline

phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50 mg samples of crude peptide were chromatographed on a Waters DELTA PAK™ C18 column (19mm x 30cm, 15m spherical) using a linear gradient: H_2O/acetonitrile 0. 1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 5 mg/ml. Peptides stored in solution were stable for an extended period of time at 4°C and could be repeatedly frozen and thawed with little apparent effect on biological activity.

The amino acid sequences of the peptides synthesized are shown in Fig. 1. DP-107 is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1 TM protein. Gallaher et al. (AIDS Res. and Human Retro. 5, 431 (1989)) and Delwart et al. (AIDS Res. and Human Reix-o. 6, 703 (1990)) observed that the primary sequence of this region was strongly predictive of a helical secondary structure and also contained a "leucine zipper" repeat. The amino terminus of the peptide was acetylated and the carboxy terminus amidated to reduce unnatural charge effects at those positions. DP-107 and each of the other peptides used in this study were purified by reverse phase HPLC and in each case the purified peptides gave a single symmetrical peak by analytical HPLC. The identity of each peptide was confirmed by electro-spray mass spectrometry, which yielded the following results: DP-107: 4526.71 (calculated 4526.31); DP-121: 4510.75 (calculated 4510.27) ; DP-116: 2057.32 (calculated 2056.44); DP-125: 4743.46 (calculated 4743.55); DP-31: 2479.35 (calculated 2480.93).

7. EXAMPLE: Evidence for Secondary Structure in Solution

Circular dichroism spectra were measured in 10 mM sodium phosphate, 150 mM sodium chloride, pH 7.0 buffer at approximately 10 mM concentrations using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrometer. Peptide concentrations were determined from A_{280} using Edlehoch's method (Biochemistry 6, 1948 (1967)).

A summary of the ultraviolet CD analyses of DP-107 is shown in Fig. 2. The results suggest a considerable amount of secondary structure for the peptide under physiologic conditions. The double minima at 222 and 208nm are characteristic of alpha helices and mean molar ellipticity values ($[Q]_{mr}$) of -32,000 at 0°C (Fig. 2A) and -27,000 at 37°C (Fig. 2B) indicate that the peptide is approximately 100% and 85% folded at these temperatures (Y. Chen et al., Biochemistry 13, 3350 (1974); N. Greenfield & G. Fasman, Biochemistry 8, 4108 (1969)). The stability of the observed structure is illustrated by the thermal melt data shown in Fig. 2C. For example, at a 10 mM concentration of DP-107, the midpoint of the melting curve (T_m) was approximately 72°C. Also apparent in Figure 2C is that the T_m for DP-107 varies as a function of peptide concentration. This concentration dependence is characteristic of leucine zipper-type structures and is indicative of stabilization of secondary structural elements by self-association (E. O'Shea et al., Science 243, 538 (1989)). Oligomerization of DP-107 in solution to form dimers and tetramers is also suggested by sedimentation equilibrium studies. Taken together, the results shown in Fig.. 2 tend to support the predictions (W. Gallaher et al., supra; E. Delwart et al., supra) that the region of gp41 corresponding to DP-107 contains a leucine zipper-like (coiled coil)

motif which may play a role in envelope oligomerization. This type of structure can be described as a homodimer formed by the specific (and often parallel) association of two alpha helices. This interaction is characterized by the alignment of the hydrophobic faces of the helices. The unusually stable secondary structure exhibited by peptides involved in these types of systems is due to these higher- order interactions. Preliminary analysis of the solution structure of DP-107 by multi-dimensional nuclear magnetic resonance (NMR) spectroscopy indicates a large number of sequential NH-NH_i crosspeaks in the NOESY spectra which is consistent with the CD evidence that under physiologic conditions, the peptide exhibits significant a-helical secondary structure.

The CD spectra of two other synthetic peptides are also shown in Fig. 2. One of these (DP-121) is identical to DP-107 but with the isoleucine at position 578 replaced with a proline residue. The other peptide, DP-116, is a 17mer and overlaps the carboxy terminus of DP-107. This peptide was synthesized to contain the same amino acids and blocking groups as CS3, a peptide described by Qureshi et al. (AIDS 4, 553 (1990)) and reported to exhibit anti-viral activity when coupled to albumin. The CD spectra observed for these two peptides indicate that both exist in random coil conformations at 37°C in direct contrast to the results obtained for DP-107. This outcome was expected for the proline substituted analogue, DP-121, in that the proline residue would tend to both break helix formation as well as disrupt hydrophobic interactions thought to stabilize coiled coil structures.

8. EXAMPLE: Reverse Transcriptase (RT) Assay

The micro RT assay was adapted from Goff et al. (J. Virol. 38, 239 (1981)) and Willey et al. (J. Virol. 62, 139 (1988)). Supernatants from virus/cell cultures are made 1% in Triton-X100. A 10ml sample of supernatant was added to 50ml of RT cocktail in a 96 well U bottom microtiter plate and the samples incubated at 370C for 90 min. The cocktail contained 75mM KCl, 2mM dithiothreitol, 5mm Mgcl2l 5mg/ml poly A (Pharmacia cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5 mM non-radioactive dTTP, and 10 mCi/ml ^{32}p-dTTP (Amersham cat. No. PB.10167). After the incubation period, 40 ml of reaction mixture was applied to a Schleicher and Schuell NA45 membrane (or DE81 paper) saturated in 2xSSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a Schleicher and Schuell Minifold over one sheet of GBOO3 filter paper. Each well of the minifold was washed four times with 200 ml 2xSSC. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally the membrane was drained on absorbent paper, placed on Whatman #3 paper, covered with saran wrap, and exposed to film overnight.

9. EXAMPLE: HIV-1 Virus Propagation

The HIV-1_{LAI} virus was obtained from R. Gallo (see M. Popovic et al., Science 224, 497 (1984)) and propagated in CEM cells cultured in RPMI 1640 containing 10% FCS. Supernatant from the infected CEM cells was passed through a 0.2 mm filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose 25 ml of serially diluted virus was

added to 75 ml AA5 cells at $2x10^5$/ml in a 96 w ll microtiter plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post infection supernatant samples were tested for virus replication as evidenced by RT activity released to the supernatant in accordance with the procedure described above. The $TCID_{50}$ was calculated according to the Reed and Muench formula in accordance with known techniques. See L. Reed et al., Amer. J. Hygiene 27, 493 (1938) . The titer of the HIV-1_{LAI} stock used for these studies, as measured on the AA5 cell line, was approximately $1x10^7TCID_{50}$/ml. The two primary isolates were obtained from PBMCs of two infected donors, one from Brazil (HIV-1_{Br3}) and the other Trinidad (HIV-1_{QZ2775}) by co-cultivation with PHA-blasted normal donor PBMCs in RPMI 1640 containing IL2. The infectious titers of the primary virus stocks were estimated by titration onto normal human PHA blasted PBMCs in a 96 well microtiter plate, again using RT activity released to the supernatant as evidence for successful infection. The infectious titer of both of these isolates was estimated to be approximately $1X10^3$ $TCID_{100}$/ml.

10. <u>EXAMPLE: Peptide Inhibition of Infected Cell Induced Syncytia Formation</u>

The initial screen for antiviral activity of the peptides shown in Fig. 1 was for blockade of syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells with chronically infected (HIV-1_{IIIB}) CEM cells.

Approximately $7x10^4$ Molt cells were incubated with $1x10^4$ CEM cells chronically infected with the HIV-1_{LAI} virus in 96 well plates (one-half area cluster

plates;Costar. Cambridge, MA) in a final volume of 100ml culture media in accordance with known techniques (T. Matthews et al., Proc. Natl. Acad. Sci. U. S. A. 84, 5424 (1987)). Peptide inhibitors were added in a volume of 10ml and the cell mixtures were incubated for 24 hr at 37°C. At that time point, multinucleated giant cells were estimated by microscopic examination at a 40x magnification which allowed visualization of the entire well in a single field.

The results of three such experiments are shown in Table 1. In the first of these, serial peptide concentrations between 50 μg/ml and 1.5 mg/ml were tested for blockade of the cell fusion process. It is shown that DP-107 afforded complete protection down to a concentration of 6 mg/ml. The overlapping 17mer peptide, DP-116, which is analogous to the previously described CS3 by Qureshi et al. (AIDS 4, 553 (1990)) exhibited no evidence of anti-fusogenic activity even at 50 mg/ml. This observation is in agreement with that study which only found anti-viral activity for CS3 after conjugation to albumin. A second peptide DP-31 representing an overlapping immunodominant site (M. Oldstone et al., J. Virol. 65, 1727 (1991); J. Wang et al., Proc. Natl. Acad. Sci. USA 83, 1659 (1986)) also failed to show inhibitory activity.

TABLE 1. Test for Peptide Blockade of HIV-1 Induced Cell-Cell Fusion

		Syncytia Number Peptide Concentration (micrograms/ml)						
	Peptide	50	25	12	6	3	1.5	0
EXP. 1	DP-31	85	80	78	87	90	75	89
	DP-116	89	82	93	92	89	82	89
	DP-107	0	0	0	0	46	80	89
		40	20	10	5	2.5	1.25	0
EXP. 2	DP-107	0	0	0	36	83	98	93
	DP-125	0	0	0	0	3	35	93
EXP. 3	DP-121	69	71	65	60	68	ND	76
	DP-125	0	0	0	0	0	0	76

The inhibitory activity of DP-107 did not appear related to cytotoxic or cytostatic effects since in other studies CEM cells grown in the presence of DP-107 at 50 mg/ml (the highest concentration tested) for three days with fresh peptide added each day displayed the same viability and growth rate as control cultures. We also found that DP-107 blocked fusion mediated by the other prototypic isolates: HIV-$1_{MN, RF,}$ and $_{SF2}$.

The concentration dependence of the CD spectra described suggests that the structure of the DP-107 is stabilized by peptide self association. In similar studies, O'Shea et al. (Science 243, 538 (1989)) reported that disulfide bridging of a peptide of the leucine zipper domain in the GCN4 protein (a transcriptional regulatory factor) to form covalently bonded homodimers stabilized the coiled coil structure. Following similar reasoning we sought to determine if the limiting effective concentration for cell fusion blockade by DP-107 might in part be related to the concentration dependence of peptide

self-association. In order to test this possibility we synthesized a DP-107 analogue with a cysteine containing "tail" which after purification could be air oxidized to yield a homodimer. The resulting peptide, DP-125, exhibited about twice the apparent molecular weight of DP-107 in SDS-PAGE under non-reducing conditions indeed suggesting that a covalently bonded homodimer was generated. In the syncytial blocking assays (Table 1 experiments 2 and 3) this analogue was, in fact, more efficacious than DP-107, requiring one-half to one-fourth the concentration for inhibition. The increased activity exhibited by DP-125 has reproduced in all assays performed to date and suggests that a dimer or higher order multimer might actually represent the biologically active form of the peptide. Also, CD measurements of DP-125 were found to yield similar ellipticity values as the parental DP-107. Taken together these observations indicate that the individual peptide components of the putative multimers are arranged in a parallel rather than anti-parallel orientation.

To gain further insights as to whether the solution structure observed for DP-107 in the CD and NMR studies is required for biological activity, the proline-containing analog (DP-121) which failed to exhibit helix related signals at 37°C in the CD experiments was tested for activity in the cell fusion assay. The results showed no sign of inhibitory activity as indicated in Table 1. Although this does not prove that structure is necessary for biological activity, it is consistent with that possibility. In a similar fashion, each of the DP-107 peptide analogues tested to date that failed to block cell fusion have also failed to show evidence of stable

solution structure in CD studies. Also, a peptide which formed a coiled coil structure (GCN4-p1, provided by R. Rutkowski) exhibited no biological activity.

11. EXAMPLE: Peptide Inhibition of Infection by Cell-Free Virus

The peptides were next tested for blockade of infection by cell-free virus. The results shown in Fig. 3 are representative of several experiments in which the DP-107, 125, and 116 (CS3) peptides were compared for potency in the blockade of HIV_{LAI}, infection of AA5 cells. Each level of peptide was incubated in triplicate with about 500 $TCID_{50}$ of virus and cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results are shown in Fig. 3 and demonstrate that both the DP-107 and DP-125 reagents inhibited the de-novo infection process at about the same effective doses as noted in the fusion assays described above. Moreover the dose required for inhibitory effect was lower for the disulfide bridged DP-125 analogue and no hint of anti-viral effect was noted for the DP-116 peptide.

12. EXAMPLE: Peptide Inhibition of PBMC Infection by Primary Isolates

It is now apparent that substantial differences in sensitivity to anti-viral agents can exist between laboratory adapted prototypic isolates and primary field isolates passaged only through PBMCs. This problem was first highlighted by Ho and colleagues (E. Dear et al., Proc. Natl. Acad. Sci. 87, 6574 (1990)) in studies with soluble CD4. To test if the gp41 peptides might exhibit a similar discordance in reactivity, the DP-107, DP-125 (cysteine analogue),

and sT4 (same reagent as used in the preceding experiment) were compared for inhibition of PBMC infection by two primary HIV-1 isolates and HIV_{LAI}. The results of these studies (Fig.5) show that the peptides inhibit both the primary and prototypic isolates tested. Only a single dose of sT4 (10 mg/ml) was included for comparative purposes and it is apparent that this reagent is substantially more active on the cell-line adapted $HIV\text{-}1_{LAI}$ virus in comparison to the two primary isolates.

13. EXAMPLE: Synthesis of DP-107 Analogs

Analogs of DP-107 were synthesized in accordance with known techniques as given in Example 1 above. Such analogs are set forth in Table 2 below.

TABLE 2. DP-107 Analogs.

DP-118	QQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKYLKDQ	(SEQ ID NO:5
DP-122	GIKQLQARILAVERYLKDQQ	(SEQ ID NO:6
DP-123	IEAQQHLLQLTVWGIKQLQARILAVERYLKDQ	(SEQ ID NO:7
DP-127	NNLLRAIEAQQHLLQLTVWGIKQLQARILAV	(SEQ ID NO:8
DP-129	NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQGGC	(SEQ ID NO:9
DP-130	CGGNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQGGC	(SEQ ID NO:10

14. EXAMPLE: Activity of DP-107 Analogs

The activity of various DP-107 analogs as described herein was tested by the syncytia assay described in Example 5 above. These data are given in Table 3 below.

TABLE 3

Peptide	[CONC]	No. Syncytia/well at peptide concentration, ug/ml on IIIB						
		40	20	10	5	2.5	1.25	0
DP116	8.0 mg/ml	77						
DP107	4.5 mg/ml	0	0	0	4	68	88	
DP118	3.9 mg/ml	0	0	77	80	78	74	
DP121	3.9 mg/ml	79						
DP122	3.4 mg/ml	73						
DP123	4.0 mg/ml	4	55	86	76	69	80	
DP125	3.1 mg/ml	0	0	0	0	0	0	
DP127	3.3 mg/ml	0	0	0	20	53	87	
DP129	3.4 mg/ml	0	0	0	0	0	0	
DP130	4.5 mg/ml	0	0	0	0	0	47	
Ctrl cells only								85

15. EXAMPLE: Biological Activity of DP-107 and Analogs Thereof

The biological activity of DP-107 and various analogs thereof in the fusion assay described in Example 5 above and the neutralization assay described in Example 6 above is summarized in Table 4 below. The quantity of compound required to produce a ninety percent reduction in number of syncytia is shown in the column marked "Fusion"; the quantity of compound required to produce a ninety percent reduction in infectivity is given in the column marked "Neutraliz". Compounds active in the fusion assay at a range between 20 and 40 4 µg/ml are considered moderately active; compounds active at a range between 10 and 20 µg/ml are considered potent; and compounds active in

an amount of less than 10 μg/ml are considered very potent.

TABLE 4

BIOLOGY OF DP-107 AND ANALOGS

			Fusion [ug/ml][1]	Neutraliz [ug/ml][2]
DP-107	(SEQ ID No: 1)	NNLLRAIEAQQGLLQLTVWGIKQLQARILAVERYLKDQ	5	10
DP-116	(SEQ ID No: 1)	LQARILAVERYLKDQQL	>40	>30
DP-121	(SEQ ID No: 4)	NNLLRAIEAQQGLLQLTVWGIKQLQARILAVERYLKDQ	>40	>30
DP-122	(SEQ ID No: 2)	GIKQLQARILAVERYLKDQQ	>40	>30
DP-123	(SEQ ID No: 6)	IEAQQGLLQLTVWGIKQLQARILAVERYLKDQ	40	>30
DP-125	(SEQ ID No: 7)	CGGNNLLRAIEAQQGLLQLTVWGIKQLQARILAVERYLKDQ	<1	2
DP-127	(SEQ ID No: 8)	NNLLRAIEAQQGLLQLTVWGIKQLQARILAV	7	23
DP-129	(SEQ ID No: 9)	NNLLRAIEAQQGLLQLTVWGIKQLQARILAVERYLKDQGGC	<1	<1
DP-130	(SEQ ID No: 10)	CGGNNLLRAIEAQQGLLQLTVWGIKQLQARILAVERYLKDQGGC	2	<1
DP-136	(SEQ ID No: 11)	CGGNNLLRAIEAQQGLLQLTVWGIKQLQARILAV	>40	>30
DP-137	(SEQ ID No: 12)	LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAV	12	12
DP-138	(SEQ ID No: 13)	CGGLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAV	>40	>30
DP-139	(SEQ ID No: 14)	NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ	>40	>30
DP-140	(SEQ ID No: 15)	NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ	17	14

[1] 90% reduction in number of syncytia (control=90)

[2] 90% reduction in infectivity

Bold letters=non-naturally occurring amino acid residues

The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

What is Claimed Is:

1. An isolated peptide comprising a DP-107 amino acid sequence listed in SEQ ID:1.

2. An isolated peptide ranging from about 14 to about 60 amino acids in length, capable of forming a heterodimer with the peptide of Claim 1.

3. The peptide of Claim 1 or 2 wherein the amino terminus of the peptide is acetylated.

4. The peptide of Claim 1 or 2 wherein the carboxy terminus of the peptide is amidated.

5. An isolated multimer of the peptide of Claim 1 or 2.

6. The multimer of Claim 5 wherein the multimer is a tetramer.

7. The multimer of Claim 5 wherein the multimer is a dimer consisting of two peptide monomers.

8. The dimer of Claim 6 wherein the monomers of the dimer are covalently bound to one another.

9. A method for inhibiting HIV-induced cell fusion comprising contacting an HIV-infected cell with an effective amount of a peptide comprising a DP-107 amino acid sequence listed in SEQ ID:1 so that the cell fusion is inhibited.

10. The method of Claim 9 wherein the HIV is HIV-1.

11. A method for inhibiting HIV-induced cell fusion comprising contacting an HIV-infected cell with an effective amount of a peptide comprising the peptide of Claim 2 so that the cell fusion is inhibited.

12. The method of Claim 11 wherein the HIV is HIV-1.

13. The method of Claim 9 wherein the peptide is present as a multimer.

14. The method of Claim 11 wherein the peptide is present as a multimer.

15. The method of Claim 13 or 14 wherein the multimer is a dimer having two peptide monomers.

16. The method of Claim 12 wherein the monomers are covalently bound to one another.

17. A method for testing compounds capable of inhibiting the ability of HIV to infect cells, comprising:

(a) contacting a test compound to a multimer of a peptide comprising a DP-107 amino acid sequence listed in SEQ ID:1; and

(b) detecting whether the test compound disrupts the multimer, the ability of the test compound to disrupt the multimer indicating the test compound is capable of inhibiting HIV infection of cells.

18. The method of Claim 17 wherein the HIV is HIV-1.

19. The method of Claim 17 wherein the multimer is a dimer or a tetramer.

20. The method of Claim 17 wherein the contacting step is carried out in an aqueous solution.

21. A method for testing compounds capable of inhibiting the ability of HIV to infect cells, comprising:

(a) contacting a test compound to a multimer of the peptide of Claim 2; and

(b) detecting whether the test compound disrupts the multimer, the ability of the test compound to disrupt the multimer indicating the test compound is capable of inhibiting HIV infection of cells.

22. The method of Claim 21 wherein the HIV is HIV-1.

23. The method of Claim 21 wherein the multimer is a dimer or a tetramer.

24. The method of Claim 21 wherein the contacting step is carried out in an aqueous solution.

25. A method for inhibiting enveloped viral infection comprising contacting an uninfected cell with an effective amount of a peptide capable of contributing to the formation of a coiled coil peptide structure so that an enveloped virus is inhibited from infecting the uninfected cell.

26. The method of Claim 25 wherein the enveloped virus is a retrovirus.

27. The method of Claim 26 wherein the retrovirus is HIV-2, HTLV-I, or HTLV-II.

28. The method of Claim 25 wherein the enveloped virus is an influenza virus.

29. The method of Claim 25 wherein the enveloped virus is a respiratory syncytial virus.

29. A method for testing compounds capable of inhibiting the ability of an enveloped virus to infect cells, comprising:

(a) contacting a test compound to a multimer of a peptide capable of contributing to the formation of a coiled coil peptide structure; and

(b) detecting whether the test compound disrupts the multimer, the ability of the test compound to disrupt the multimer indicating the test compound is capable of inhibiting enveloped viral infection of cells.

30. The method of Claim 29 wherein the enveloped virus is a retrovirus.

31. The method of Claim 30 wherein the retrovirus is HIV-2, HTLV-I, or HTLV-II.

32. The method of Claim 29 wherein the enveloped virus is an influenza virus.

33. The method of Claim 29 wherein the multimer is a dimer or a tetramer.

34. The method of Claim 29 wherein the contacting step is carried out in an aqueous solution.

```
            550'                                                    609'
              |                                                        |
ρ-107       NNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ
ρ-121       NNLLRAIEAQQHLLQLTVWGPKQLQARILAVERYLKDQ
ρ-125    CGGNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ

ρ-31                                  ERYLKDQQLLGIWGCSCKLICG
ρ-116                        LQARILAVERYLKDQQQ
```

Fig 1

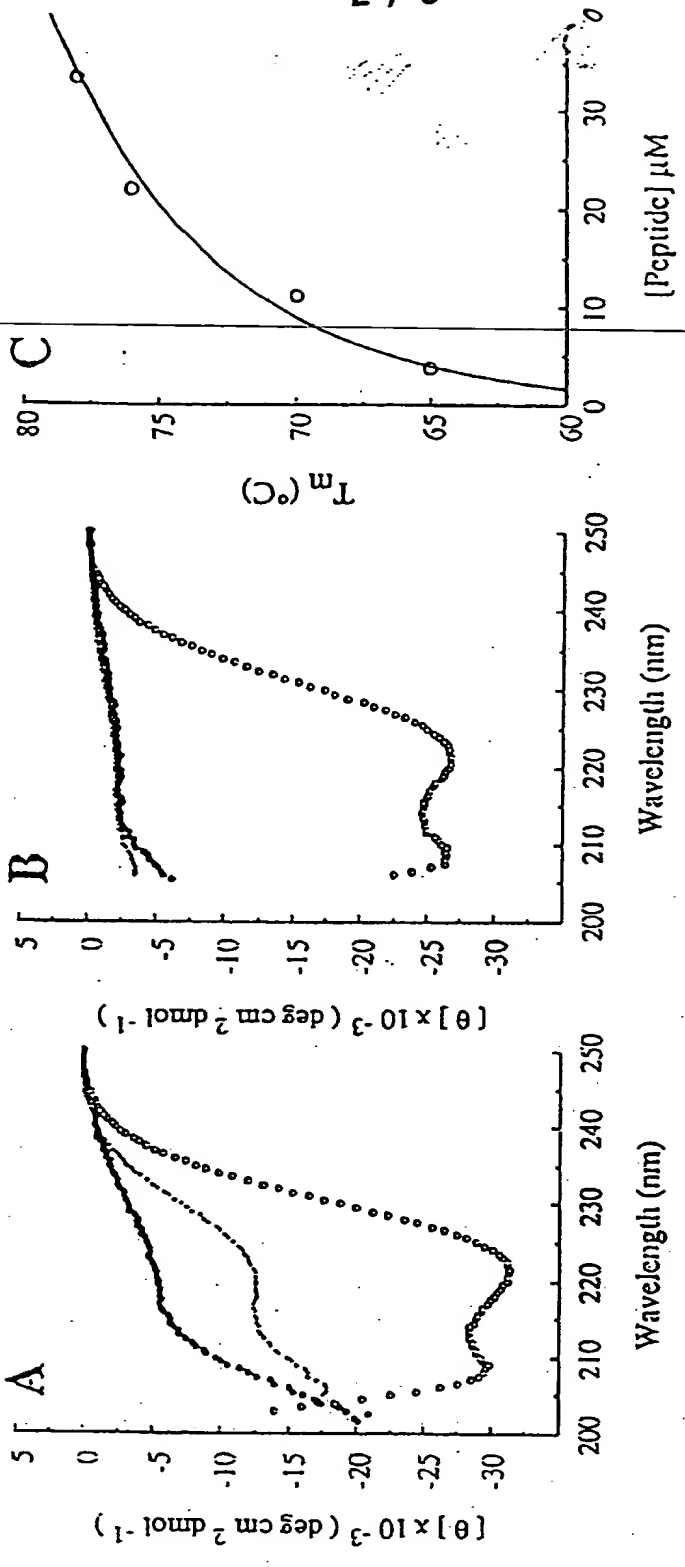

Fig 2.

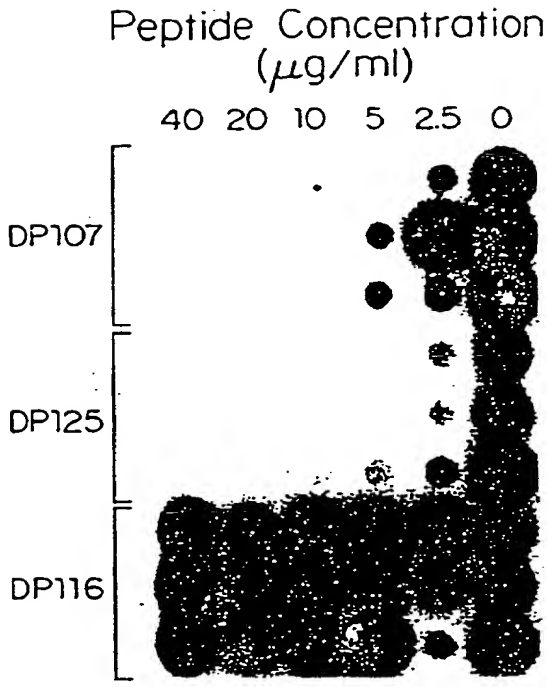

Fig 3.

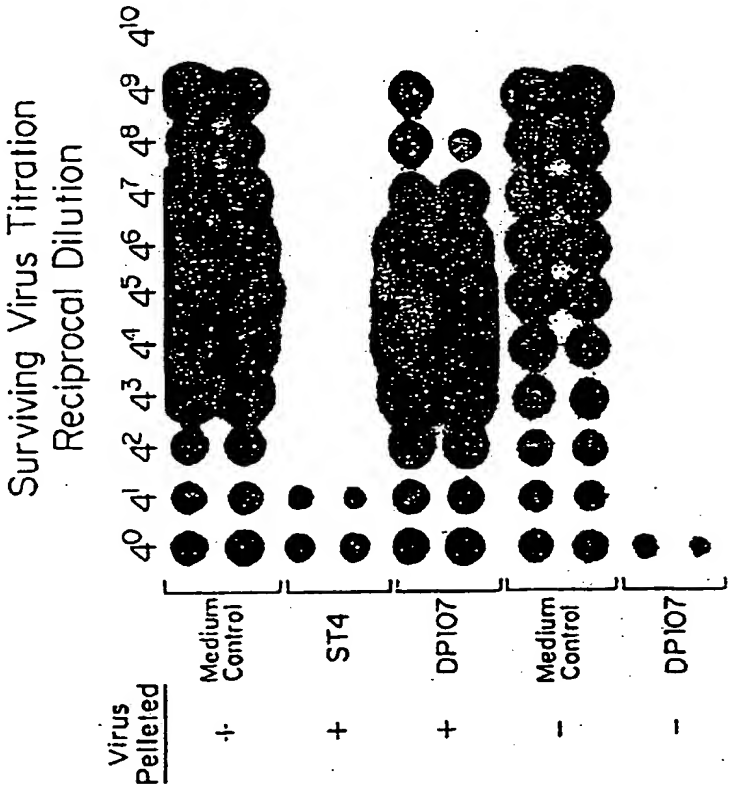
Surviving Virus Titration
Reciprocal Dilution
4^0 4^1 4^2 4^3 4^4 4^5 4^6 4^7 4^8 4^9 4^{10}
Virus Pelleted
+ Medium Control
+ ST4
+ DP107
- Medium Control
- DP107

Fig 4

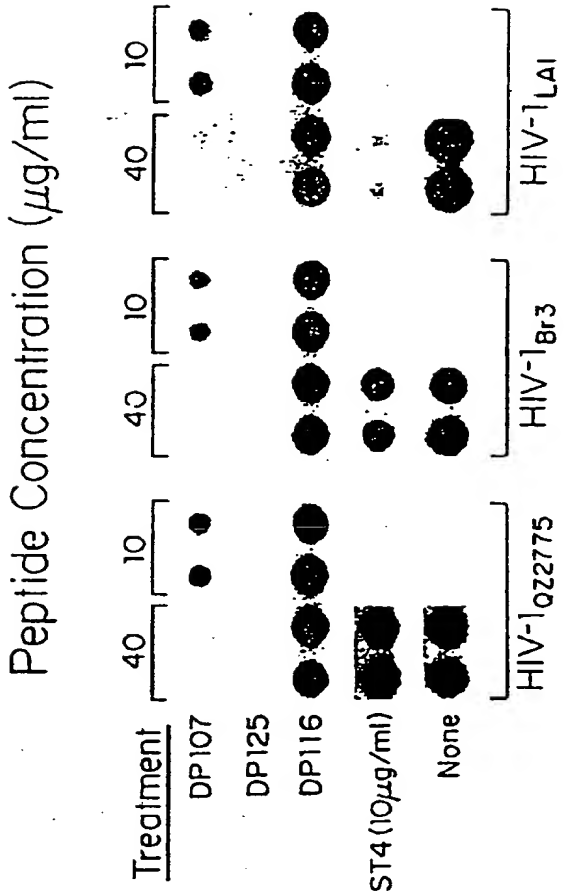
Peptide Concentration (μg/ml)
Treatment
DP107
DP125
DP116
ST4 (10μg/ml)
None
40
10
40
10
40
10
HIV-1QZ2775
HIV-1Br3
HIV-1LAI

Fig 5

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/06769

A. CLASSIFICATION P SUBJECT MATTER

IPC(5) :C07K 07/00, A61K 37/02
US CL :514/012; 530/324
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 514/012; 530/324

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

CAS ONLINE, MEDLINE, APS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	AIDS Research and Human Retroviruses, Volume 5, Number 4, issued 1989, Gallaher et al. "A General Model for the Transmembrane Proteins of HIV and Other Retroviruses", pages 431-440, see entire document.	1-8
Y	AIDS Research and Human Retroviruses, Volume 6, Number 6, issued 1990, Delwart et al., "Retroviral Envelope Glycoproteins Contain a 'Leucine Zipper'-like Repeat", pages 703-706, see entire document.	1-8

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be part of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 September 1993	OCT 05 1993
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. NOT APPLICABLE	Authorized officer MERRELL C. CASHION Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/06769

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	The Journal of General Virology, Volume 73, Part 7, issued July 1992, Buckland et al., "A Leucine Zipper Structure Present in the Measles Virus Fusion Protein is not Required for its Tetramerization but is not Essential for Fusion", pages 1703-1707, see the abstract.	1-8